

## CLAIMS

*what is claimed is:*

1. A method of analyzing a collection of genetically modified cell strains that are congenic with a parent strain, the method comprising:

(a) receiving images of phenotypes for each of the genetically modified cell strains;

(b) analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) comparing the quantitative representations of the phenotypes with (i) each other, (ii) a qualitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains.

2. The method of claim 1, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

3. The method of claim 2, wherein the deletion mutants each lack a single gene present in the parent strain.

4. The method of claim 3, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

5. The method of claim 4, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

6. The method of claim 5, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae*.

7. The method of claim 1, further comprising:  
marking one or more cell features of the genetically modified cell strains so that said features can be highlighted in the images of the phenotypes; and  
imaging the genetically modified cell strains to produce the images of the phenotypes, wherein the cell features are highlighted in the images of the phenotypes.

8. The method of claim 7, wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features comprises staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material,  
5 and a third stain for the cytoskeleton.

9. The method of claim 8, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

10. The method of claim 1, wherein analyzing the images comprises:  
receiving the intensity versus position data from one or markers on the  
genetically modified cell strains;  
quantifying geometrical information about said markers; and  
quantifying biological information about said genetically modified cell strains.

11. The method of claim 10, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

12. The method of claim 1, wherein comparing the quantitative representations of the phenotypes comprises comparing the quantitative representations of the phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

13. The method of claim 1, wherein comparing the quantitative representations of the phenotypes comprises comparing the quantitative representations of the phenotypes with a quantitative representation of a phenotype of the cell that is genetically similar or identical to one or more of the cell strains, and wherein the cell that is genetically similar or identical has been treated with a drug or  
a drug candidate.

14. The method of claim 1, further comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

15. The method of claim 14, further comprising linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

16. A computer program product comprising a machine readable medium on which is provided program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain, the instructions comprising:

(a) code for receiving images of phenotypes for each of the genetically modified cell strains;

(b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) code for comparing the quantitative representations of the phenotypes with (i) each other, (ii) a qualitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains.

17. The computer program product of claim 16, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

18. The computer program product of claim 17, wherein the deletion mutants each lack a single gene present in the parent strain.

19. The computer program product of claim 18, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

20. The computer program product of claim 19, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

21. The computer program product of claim 20, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae*.

22. The computer program product of claim 16, further comprising:  
code for imaging the genetically modified cell strains to produce the images of the phenotypes, wherein one or more cell features are highlighted by marking in the images of the phenotypes.

23. The computer program product of claim 22, wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features was accomplished by staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton.

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24. The computer program product of claim 23, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

25. The computer program product of claim 16, wherein the code for  
10 analyzing the images comprises:  
code for receiving the intensity versus position data from one or markers on  
the genetically modified cell strains;  
code for quantifying geometrical information about said markers; and  
code for quantifying biological information about said genetically modified  
15 cell strains.

26. The computer program product of claim 25, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

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27. The computer program product of claim 16, wherein the code for  
comparing the quantitative representations of the phenotypes comprises code for  
comparing the quantitative representations of the phenotypes with each other to  
cluster the phenotypes and identify common functional traits shared between multiple  
25 genetic modifications.

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28. The computer program product of claim 16, wherein the code for  
comparing the quantitative representations of the phenotypes comprises code for  
comparing the quantitative representations of the phenotypes with a quantitative  
30 representation of a phenotype of the cell that is genetically similar or identical to one  
or more of the cell strains, and wherein the cell that is genetically similar or identical  
has been treated with a drug or a drug candidate.

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29. The computer program product of claim 16, further code for comprising  
35 generating a database including records identifying the phenotypes and the  
quantitative representations of the phenotypes.

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30. The computer program product of claim 29, further comprising code for linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

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31. A computing device comprising a memory device configured to store at least temporarily program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain, the instructions comprising:

- 10 (a) code for receiving images of phenotypes for each of the genetically modified cell strains;
- (b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and
- 15 (c) code for comparing the quantitative representations of the phenotypes with (i) each other, (ii) a qualitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains.